

Detlef Weigel

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

439
papers

68,576
citations

126
h-index

256
g-index

584
ext. papers

80,571
ext. citations

14.2
avg, IF

7.79
L-index

#	Paper	IF	Citations
439	Mutation bias reflects natural selection in <i>Arabidopsis thaliana</i> .. <i>Nature</i> , 2022 ,	50.4	17
438	Chromosome-level <i>Thlaspi arvense</i> genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates.. <i>Plant Biotechnology Journal</i> , 2022 ,	11.6	2
437	Rapid genomic convergent evolution in experimental populations of Trinidadian guppies ().. <i>Evolution Letters</i> , 2022 , 6, 149-161	5.3	0
436	Commensal <i>Pseudomonas</i> strains facilitate protective response against pathogens in the host plant.. <i>Nature Ecology and Evolution</i> , 2022 ,	12.3	3
435	Genotyping-by-sequencing-based identification of <i>Arabidopsis</i> pattern recognition receptor RLP32 recognizing proteobacterial translation initiation factor IF1.. <i>Nature Communications</i> , 2022 , 13, 1294	17.4	1
434	HASTY modulates miRNA biogenesis by linking pri-miRNA transcription and processing. <i>Molecular Plant</i> , 2021 , 14, 426-439	14.4	20
433	Population structure and evolution of resistance to acetolactate synthase (ALS)-inhibitors in <i>Amaranthus tuberculatus</i> in Italy. <i>Pest Management Science</i> , 2021 , 77, 2971-2980	4.6	2
432	Genetic Mapping by Sequencing More Precisely Detects Loci Responsible for Anaerobic Germination Tolerance in Rice. <i>Plants</i> , 2021 , 10,	4.5	2
431	Drainage-structuring of ancestral variation and a common functional pathway shape limited genomic convergence in natural high- and low-predation guppies. <i>PLoS Genetics</i> , 2021 , 17, e1009566	6	6
430	The genetic architecture and population genomic signatures of glyphosate resistance in <i>Amaranthus tuberculatus</i> . <i>Molecular Ecology</i> , 2021 , 30, 5373-5389	5.7	6
429	A Truncated Singleton NLR Causes Hybrid Necrosis in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021 , 38, 557-574	8.3	12
428	Male-specific Y-chromosomal regions in waterhemp (<i>Amaranthus tuberculatus</i>) and Palmer amaranth (<i>Amaranthus palmeri</i>). <i>New Phytologist</i> , 2021 , 229, 3522-3533	9.8	2
427	The population genomics of adaptive loss of function. <i>Heredity</i> , 2021 , 126, 383-395	3.6	5
426	Plant NLR diversity: the known unknowns of pan-NLRomes. <i>Plant Cell</i> , 2021 , 33, 814-831	11.6	15
425	Host-associated microbe PCR (hamPCR) enables convenient measurement of both microbial load and community composition. <i>ELife</i> , 2021 , 10,	8.9	4
424	One Hundred Years of Hybrid Necrosis: Hybrid Autoimmunity as a Window into the Mechanisms and Evolution of Plant-Pathogen Interactions. <i>Annual Review of Phytopathology</i> , 2021 , 59, 213-237	10.8	2
423	The EDS1-PAD4-ADR1 node mediates <i>Arabidopsis</i> pattern-triggered immunity. <i>Nature</i> , 2021 , 598, 495-499	90.4	28

422	Multiple Sources of Introduction of North American <i>Arabidopsis thaliana</i> from across Eurasia. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5328-5344	8.3	0
421	CRISPR-finder: A high throughput and cost-effective method to identify successfully edited <i>Arabidopsis thaliana</i> individuals 2021 , 2,		1
420	Combining whole-genome shotgun sequencing and rRNA gene amplicon analyses to improve detection of microbe-microbe interaction networks in plant leaves. <i>ISME Journal</i> , 2020 , 14, 2116-2130	11.9	27
419	What natural variation can teach us about resistance durability. <i>Current Opinion in Plant Biology</i> , 2020 , 56, 89-98	9.9	6
418	Atypical Resistance Protein RPW8/HR Triggers Oligomerization of the NLR Immune Receptor RPP7 and Autoimmunity. <i>Cell Host and Microbe</i> , 2020 , 27, 405-417.e6	23.4	39
417	Tropical Trees as Time Capsules of Anthropogenic Activity. <i>Trends in Plant Science</i> , 2020 , 25, 369-380	13.1	11
416	Blue Native Polyacrylamide Gel Electrophoresis (BN-PAGE) for the Analysis of Protein Oligomers in Plants. <i>Current Protocols in Plant Biology</i> , 2020 , 5, e20107	2.8	5
415	Identifying genetic variants underlying phenotypic variation in plants without complete genomes. <i>Nature Genetics</i> , 2020 , 52, 534-540	36.3	46
414	AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2020 , 48, D1063-D1068	20.1	18
413	A new role for histone demethylases in the maintenance of plant genome integrity. <i>ELife</i> , 2020 , 9,	8.9	12
412	The Earth BioGenome project: opportunities and challenges for plant genomics and conservation. <i>Plant Journal</i> , 2020 , 102, 222-229	6.9	17
411	Draft Genomes of <i>Amaranthus tuberculatus</i> , <i>Amaranthus hybridus</i> , and <i>Amaranthus palmeri</i> . <i>Genome Biology and Evolution</i> , 2020 , 12, 1988-1993	3.9	16
410	Improved Reference Genome Uncovers Novel Sex-Linked Regions in the Guppy (<i>Poecilia reticulata</i>). <i>Genome Biology and Evolution</i> , 2020 , 12, 1789-1805	3.9	18
409	RST1 and RIPR connect the cytosolic RNA exosome to the Ski complex in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2019 , 10, 3871	17.4	25
408	Natural selection on the <i>Arabidopsis thaliana</i> genome in present and future climates. <i>Nature</i> , 2019 , 573, 126-129	50.4	63
407	NCP activates chloroplast transcription by controlling phytochrome-dependent dual nuclear and plastidial switches. <i>Nature Communications</i> , 2019 , 10, 2630	17.4	20
406	Phytochrome activates the plastid-encoded RNA polymerase for chloroplast biogenesis via nucleus-to-plastid signaling. <i>Nature Communications</i> , 2019 , 10, 2629	17.4	26
405	Nonlinear phenotypic variation uncovers the emergence of heterosis in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2019 , 17, e3000214	9.7	19

404	Arabidopsis FLL2 promotes liquid-liquid phase separation of polyadenylation complexes. <i>Nature</i> , 2019 , 569, 265-269	50.4	86
403	Transmission ratio distortion is frequent in Arabidopsis thaliana controlled crosses. <i>Heredity</i> , 2019 , 122, 294-304	3.6	11
402	A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. <i>Cell</i> , 2019 , 178, 1260-1272.e14	16.2	125
401	RPW8/HR repeats control NLR activation in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2019 , 15, e1008313	6	39
400	Sequence and Expression Differences Underlie Functional Specialization of Arabidopsis MicroRNAs miR159 and miR319. <i>Developmental Cell</i> , 2019 , 51, 129	10.2	3
399	Long-term balancing selection drives evolution of immunity genes in. <i>ELife</i> , 2019 , 8,	8.9	31
398	Author response: Long-term balancing selection drives evolution of immunity genes in Capsella 2019 ,		2
397	Multiple modes of convergent adaptation in the spread of glyphosate-resistant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 21076-21084	11.5	53
396	An Ultra High-Density Crossover Map That Refines the Influences of Structural Variation and Epigenetic Features. <i>Genetics</i> , 2019 , 213, 771-787	4	42
395	Fine-Grained Analysis of Spontaneous Mutation Spectrum and Frequency in. <i>Genetics</i> , 2019 , 211, 703-714	4	46
394	Comparing Arabidopsis receptor kinase and receptor protein-mediated immune signaling reveals BIK1-dependent differences. <i>New Phytologist</i> , 2019 , 221, 2080-2095	9.8	41
393	EFFECTOR OF TRANSCRIPTION Factors are novel plant-specific regulators associated with genomic DNA methylation in Arabidopsis. <i>New Phytologist</i> , 2019 , 221, 261-278	9.8	4
392	Genome-wide signatures of flowering adaptation to climate temperature: Regional analyses in a highly diverse native range of Arabidopsis thaliana. <i>Plant, Cell and Environment</i> , 2018 , 41, 1806-1820	8.4	28
391	High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018 , 9, 541	17.4	164
390	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. <i>Nature Genetics</i> , 2018 , 50, 285-296	36.3	229
389	Genomic basis and evolutionary potential for extreme drought adaptation in Arabidopsis thaliana. <i>Nature Ecology and Evolution</i> , 2018 , 2, 352-358	12.3	89
388	Complex Relationships between Chromatin Accessibility, Sequence Divergence, and Gene Expression in Arabidopsis thaliana. <i>Molecular Biology and Evolution</i> , 2018 , 35, 837-854	8.3	23
387	The AraGWAS Catalog: a curated and standardized Arabidopsis thaliana GWAS catalog. <i>Nucleic Acids Research</i> , 2018 , 46, D1150-D1156	20.1	39

386	Adaptive diversification of growth allometry in the plant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 3416-3421	11.5	40
385	The MicroRNA miR773 Is Involved in the Arabidopsis Immune Response to Fungal Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2018 , 31, 249-259	3.6	30
384	Dose-dependent interactions between two loci trigger altered shoot growth in BG-5 × Krotzenburg-0 (Kro-0) hybrids of Arabidopsis thaliana. <i>New Phytologist</i> , 2018 , 217, 392-406	9.8	8
383	Arabidopsis thaliana and Pseudomonas Pathogens Exhibit Stable Associations over Evolutionary Timescales. <i>Cell Host and Microbe</i> , 2018 , 24, 168-179.e4	23.4	73
382	Genetic Control of Floral Induction and Floral Patterning 2018 , 315-348		
381	An efficient CRISPR vector toolbox for engineering large deletions in. <i>Plant Methods</i> , 2018 , 14, 65	5.8	36
380	Image-based methods for phenotyping growth dynamics and fitness components in. <i>Plant Methods</i> , 2018 , 14, 63	5.8	29
379	The rate and potential relevance of new mutations in a colonizing plant lineage. <i>PLoS Genetics</i> , 2018 , 14, e1007155	6	65
378	A Role for the F-Box Protein HAWAIIAN SKIRT in Plant microRNA Function. <i>Plant Physiology</i> , 2018 , 176, 730-741	6.6	18
377	Modulation of ACD6 dependent hyperimmunity by natural alleles of an Arabidopsis thaliana NLR resistance gene. <i>PLoS Genetics</i> , 2018 , 14, e1007628	6	17
376	Partial maintenance of organ-specific epigenetic marks during plant asexual reproduction leads to heritable phenotypic variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9145-E9152	11.5	28
375	DNA sequence properties that predict susceptibility to epiallelic switching. <i>EMBO Journal</i> , 2017 , 36, 617-628	15.2	39
374	On the post-glacial spread of human commensal Arabidopsis thaliana. <i>Nature Communications</i> , 2017 , 8, 14458	17.4	41
373	Activation of a Plant NLR Complex through Heteromeric Association with an Autoimmune Risk Variant of Another NLR. <i>Current Biology</i> , 2017 , 27, 1148-1160	6.3	53
372	Arabidopsis proteins with a transposon-related domain act in gene silencing. <i>Nature Communications</i> , 2017 , 8, 15122	17.4	16
371	A single haplotype hyposensitive to light and requiring strong vernalization dominates Arabidopsis thaliana populations in Patagonia, Argentina. <i>Molecular Ecology</i> , 2017 , 26, 3389-3404	5.7	6
370	The Arabidopsis miR396 mediates pathogen-associated molecular pattern-triggered immune responses against fungal pathogens. <i>Scientific Reports</i> , 2017 , 7, 44898	4.9	64
369	Chlorosis caused by two recessively interacting genes reveals a role of RNA helicase in hybrid breakdown in Arabidopsis thaliana. <i>Plant Journal</i> , 2017 , 91, 251-262	6.9	18

368	Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. <i>Scientific Reports</i> , 2017 , 7, 482	4.9	357
367	AraPheno: a public database for Arabidopsis thaliana phenotypes. <i>Nucleic Acids Research</i> , 2017 , 45, D1054-D1058	4.8	15
366	Forever Young: The Role of Ubiquitin Receptor DA1 and E3 Ligase BIG BROTHER in Controlling Leaf Growth and Development. <i>Plant Physiology</i> , 2017 , 173, 1269-1282	6.6	24
365	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. <i>Plant Cell</i> , 2017 , 29, 5-19	11.6	56
364	Altered chromatin compaction and histone methylation drive non-additive gene expression in an interspecific Arabidopsis hybrid. <i>Genome Biology</i> , 2017 , 18, 157	18.3	55
363	Prominent topologically associated domains differentiate global chromatin packing in rice from Arabidopsis. <i>Nature Plants</i> , 2017 , 3, 742-748	11.5	121
362	SPF45-related splicing factor for phytochrome signaling promotes photomorphogenesis by regulating pre-mRNA splicing in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E7018-E7027	11.5	36
361	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. <i>Science</i> , 2017 , 357, 512-515	33.3	110
360	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017 , 49, 1099-1106	36.3	421
359	What causes mating system shifts in plants? Arabidopsis lyrata as a case study. <i>Heredity</i> , 2017 , 118, 52-63	3.6	21
358	Methods for Genotyping-by-Sequencing. <i>Methods in Molecular Biology</i> , 2017 , 1492, 221-242	1.4	27
357	Novel allelic variants in ACD6 cause hybrid necrosis in local collection of Arabidopsis thaliana. <i>New Phytologist</i> , 2017 , 213, 900-915	9.8	31
356	Natural Variation of Molecular and Morphological Gibberellin Responses. <i>Plant Physiology</i> , 2017 , 173, 703-714	6.6	10
355	Effector-Triggered Immune Response in Arabidopsis thaliana Is a Quantitative Trait. <i>Genetics</i> , 2016 , 204, 337-53	4	29
354	Sequencing of the genus Arabidopsis identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016 , 48, 1077-82	36.3	134
353	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016 , 166, 492-505	56.2	353
352	Genetic architecture of nonadditive inheritance in Arabidopsis thaliana hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7317-E7326	11.5	36
351	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , 2016 , 166, 481-491	40.1	620

350	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016 , 48, 109-11	36.3	148
349	Epigenome confrontation triggers immediate reprogramming of DNA methylation and transposon silencing in <i>Arabidopsis thaliana</i> F1 epihybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E2083-92	11.5	59
348	A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , 2016 , 28, 606-9	11.6	25
347	Microbial Hub Taxa Link Host and Abiotic Factors to Plant Microbiome Variation. <i>PLoS Biology</i> , 2016 , 14, e1002352	9.7	588
346	Cooperation and Conflict in the Plant Immune System. <i>PLoS Pathogens</i> , 2016 , 12, e1005452	7.6	36
345	Hyperosmotic stress memory in <i>Arabidopsis</i> is mediated by distinct epigenetically labile sites in the genome and is restricted in the male germline by DNA glycosylase activity. <i>ELife</i> , 2016 , 5,	8.9	183
344	The Genome of the Trinidadian Guppy, <i>Poecilia reticulata</i> , and Variation in the Guanapo Population. <i>PLoS ONE</i> , 2016 , 11, e0169087	3.7	57
343	Gene silencing pathways found in the green alga <i>Volvox carteri</i> reveal insights into evolution and origins of small RNA systems in plants. <i>BMC Genomics</i> , 2016 , 17, 853	4.5	9
342	Why I Love Genetics: Essay on Occasion of Being Awarded the GSA Medal 2016. <i>Genetics</i> , 2016 , 204, 841-843	4.4	843
341	Genome-wide analysis of chromatin packing in <i>Arabidopsis thaliana</i> at single-gene resolution. <i>Genome Research</i> , 2016 , 26, 1057-68	9.7	124
340	Allelochemicals of the phenoxazinone class act at physiologically relevant concentrations. <i>Plant Signaling and Behavior</i> , 2016 , 11, e1176818	2.5	4
339	Mutant Allele-Specific Uncoupling of PENETRATION3 Functions Reveals Engagement of the ATP-Binding Cassette Transporter in Distinct Tryptophan Metabolic Pathways. <i>Plant Physiology</i> , 2015 , 168, 814-27	6.6	53
338	Century-scale methylome stability in a recently diverged <i>Arabidopsis thaliana</i> lineage. <i>PLoS Genetics</i> , 2015 , 11, e1004920	6	104
337	Rapid and inexpensive whole-genome genotyping-by-sequencing for crossover localization and fine-scale genetic mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 385-98	3.2	77
336	Beyond the thale: comparative genomics and genetics of <i>Arabidopsis</i> relatives. <i>Nature Reviews Genetics</i> , 2015 , 16, 285-98	30.1	64
335	Ubiquitin facilitates a quality-control pathway that removes damaged chloroplasts. <i>Science</i> , 2015 , 350, 450-4	33.3	117
334	Population Genomics for Understanding Adaptation in Wild Plant Species. <i>Annual Review of Genetics</i> , 2015 , 49, 315-38	14.5	58
333	Chromatin in 3D: progress and prospects for plants. <i>Genome Biology</i> , 2015 , 16, 170	18.3	45

332	Salinity Is an Agent of Divergent Selection Driving Local Adaptation of Arabidopsis to Coastal Habitats. <i>Plant Physiology</i> , 2015 , 168, 915-29	6.6	29
331	Population genomics of natural and experimental populations of guppies (<i>Poecilia reticulata</i>). <i>Molecular Ecology</i> , 2015 , 24, 389-408	5.7	59
330	Genome-wide analysis of local chromatin packing in Arabidopsis thaliana. <i>Genome Research</i> , 2015 , 25, 246-56	9.7	181
329	Genome expansion of Arabis alpina linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015 , 1, 14023	11.5	121
328	Adenylate cyclase 5 is required for melanophore and male pattern development in the guppy (<i>Poecilia reticulata</i>). <i>Pigment Cell and Melanoma Research</i> , 2015 , 28, 545-58	4.5	3
327	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. <i>Plant Journal</i> , 2015 , 83, 189-212	6.9	136
326	Modulation of Ambient Temperature-Dependent Flowering in Arabidopsis thaliana by Natural Variation of FLOWERING LOCUS M. <i>PLoS Genetics</i> , 2015 , 11, e1005588	6	61
325	Improving the Annotation of Arabidopsis lyrata Using RNA-Seq Data. <i>PLoS ONE</i> , 2015 , 10, e0137391	3.7	50
324	Plants Release Precursors of Histone Deacetylase Inhibitors to Suppress Growth of Competitors. <i>Plant Cell</i> , 2015 , 27, 3175-89	11.6	48
323	Rapid divergence and high diversity of miRNAs and miRNA targets in the Camelinaeae. <i>Plant Journal</i> , 2015 , 81, 597-610	6.9	19
322	Dissection of miRNA pathways using arabidopsis mesophyll protoplasts. <i>Molecular Plant</i> , 2015 , 8, 261-75	14.4	16
321	Mutations in the EDR1 Gene Alter the Response of Arabidopsis thaliana to Phytophthora infestans and the Bacterial PAMPs flg22 and elf18. <i>Molecular Plant-Microbe Interactions</i> , 2015 , 28, 122-33	3.6	9
320	Evolution. Response to Comment on "A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity". <i>Science</i> , 2015 , 347, 621	33.3	4
319	Plant genetic archaeology: whole-genome sequencing reveals the pedigree of a classical trisomic line. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 5, 253-9	3.2	3
318	A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. <i>Science</i> , 2014 , 343, 645-8	33.3	94
317	Species-wide genetic incompatibility analysis identifies immune genes as hot spots of deleterious epistasis. <i>Cell</i> , 2014 , 159, 1341-51	56.2	184
316	Structural features determining flower-promoting activity of Arabidopsis FLOWERING LOCUS T. <i>Plant Cell</i> , 2014 , 26, 552-64	11.6	137
315	A functional and evolutionary perspective on transcription factor binding in Arabidopsis thaliana. <i>Plant Cell</i> , 2014 , 26, 3894-910	11.6	73

3 ¹⁴	Temporal control of leaf complexity by miRNA-regulated licensing of protein complexes. <i>Current Biology</i> , 2014 , 24, 2714-9	6.3	109
3 ¹³	Trowel: a fast and accurate error correction module for Illumina sequencing reads. <i>Bioinformatics</i> , 2014 , 30, 3264-5	7.2	18
3 ¹²	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014 , 46, 1034-8	36.3	269
3 ¹¹	Mating system shifts and transposable element evolution in the plant genus <i>Capsella</i> . <i>BMC Genomics</i> , 2014 , 15, 602	4.5	41
3 ¹⁰	Convergent targeting of a common host protein-network by pathogen effectors from three kingdoms of life. <i>Cell Host and Microbe</i> , 2014 , 16, 364-75	23.4	242
3 ⁰⁹	Transcriptome assemblies for studying sex-biased gene expression in the guppy, <i>Poecilia reticulata</i> . <i>BMC Genomics</i> , 2014 , 15, 400	4.5	53
3 ⁰⁸	Multiple pigment cell types contribute to the black, blue, and orange ornaments of male guppies (<i>Poecilia reticulata</i>). <i>PLoS ONE</i> , 2014 , 9, e85647	3.7	25
3 ⁰⁷	Evolution of DNA methylation patterns in the Brassicaceae is driven by differences in genome organization. <i>PLoS Genetics</i> , 2014 , 10, e1004785	6	125
3 ⁰⁶	DNA topoisomerase 1 promotes transcriptional silencing of transposable elements through DNA methylation and histone lysine 9 dimethylation in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004446	6	16
3 ⁰⁵	Analysis of a plant complex resistance gene locus underlying immune-related hybrid incompatibility and its occurrence in nature. <i>PLoS Genetics</i> , 2014 , 10, e1004848	6	43
3 ⁰⁴	Activation of the <i>Arabidopsis thaliana</i> immune system by combinations of common ACD6 alleles. <i>PLoS Genetics</i> , 2014 , 10, e1004459	6	46
3 ⁰³	Mining herbaria for plant pathogen genomes: back to the future. <i>PLoS Pathogens</i> , 2014 , 10, e1004028	7.6	50
3 ⁰²	Regulation of pri-miRNA processing by the hnRNP-like protein AtGRP7 in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2014 , 42, 9925-36	20.1	59
3 ⁰¹	New <i>Arabidopsis</i> advanced intercross recombinant inbred lines reveal female control of nonrandom mating. <i>Plant Physiology</i> , 2014 , 165, 175-85	6.6	13
3 ⁰⁰	CHOLINE TRANSPORTER-LIKE1 is required for sieve plate development to mediate long-distance cell-to-cell communication. <i>Nature Communications</i> , 2014 , 5, 4276	17.4	52
2 ⁹⁹	Different mechanisms for <i>Arabidopsis thaliana</i> hybrid necrosis cases inferred from temperature responses. <i>Plant Biology</i> , 2014 , 16, 1033-41	3.7	10
2 ⁹⁸	Targeted mutagenesis in the model plant <i>Nicotiana benthamiana</i> using Cas9 RNA-guided endonuclease. <i>Nature Biotechnology</i> , 2013 , 31, 691-3	44.5	742
2 ⁹⁷	Accurate indel prediction using paired-end short reads. <i>BMC Genomics</i> , 2013 , 14, 132	4.5	22

296	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E2655-62	11.5	260
295	Pigment pattern formation in the guppy, <i>Poecilia reticulata</i> , involves the Kita and Csf1ra receptor tyrosine kinases. <i>Genetics</i> , 2013 , 194, 631-46	4	37
294	Kontrolle der Pflanzenentwicklung durch MikroRNAs. <i>BioSpektrum</i> , 2013 , 19, 622-624	0.1	
293	Sixty years of genome biology. <i>Genome Biology</i> , 2013 , 14, 113	18.3	4
292	Artificial microRNAs for specific gene silencing in rice. <i>Methods in Molecular Biology</i> , 2013 , 956, 131-49	1.4	5
291	Functional analysis of splice variant expression of MADS AFFECTING FLOWERING 2 of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2013 , 81, 57-69	4.6	52
290	Impaired sterol ester synthesis alters the response of <i>Arabidopsis thaliana</i> to <i>Phytophthora infestans</i> . <i>Plant Journal</i> , 2013 , 73, 456-68	6.9	38
289	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013 , 45, 831-5	36.3	274
288	Coordination of flower maturation by a regulatory circuit of three microRNAs. <i>PLoS Genetics</i> , 2013 , 9, e1003374	6	84
287	Transposon variants and their effects on gene expression in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003265	6.5	94
286	LNK genes integrate light and clock signaling networks at the core of the <i>Arabidopsis</i> oscillator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12120-5	11.5	118
285	Tissue-specific silencing of <i>Arabidopsis</i> SU(VAR)3-9 HOMOLOG8 by miR171a. <i>Plant Physiology</i> , 2013 , 161, 805-12	6.6	46
284	User guide for mapping-by-sequencing in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2013 , 14, R61	18.3	82
283	The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2013 , 2, e00731	8.9	246
282	Genome-wide identification of KANADI1 target genes. <i>PLoS ONE</i> , 2013 , 8, e77341	3.7	42
281	The genomic landscape of meiotic crossovers and gene conversions in <i>Arabidopsis thaliana</i> . <i>ELife</i> , 2013 , 2, e01426	8.9	149
280	Circadian clock adjustment to plant iron status depends on chloroplast and phytochrome function. <i>EMBO Journal</i> , 2013 , 32, 511-23	13	64
279	Author response: The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine 2013 ,		7

278	The eLife approach to peer review. <i>ELife</i> , 2013 , 2, e00799	8.9	16
277	A year in the life of eLife. <i>ELife</i> , 2013 , 2, e01516	8.9	4
276	eLife and early career researchers. <i>ELife</i> , 2013 , 2, e01633	8.9	0
275	Natural variation in biogenesis efficiency of individual <i>Arabidopsis thaliana</i> microRNAs. <i>Current Biology</i> , 2012 , 22, 166-70	6.3	39
274	Fitness of <i>Arabidopsis thaliana</i> mutation accumulation lines whose spontaneous mutations are known. <i>Evolution; International Journal of Organic Evolution</i> , 2012 , 66, 2335-9	3.8	35
273	MIGS: miRNA-induced gene silencing. <i>Plant Journal</i> , 2012 , 70, 541-7	6.9	69
272	Synteny-based mapping-by-sequencing enabled by targeted enrichment. <i>Plant Journal</i> , 2012 , 71, 517-266.9		31
271	The recombination landscape in <i>Arabidopsis thaliana</i> F2 populations. <i>Heredity</i> , 2012 , 108, 447-55	3.6	112
270	Fast-forward genetics identifies plant CPL phosphatases as regulators of miRNA processing factor HYL1. <i>Cell</i> , 2012 , 151, 859-870	56.2	171
269	Epigenetic variation: origin and transgenerational inheritance. <i>Current Opinion in Plant Biology</i> , 2012 , 15, 562-7	9.9	89
268	Epialleles in plant evolution. <i>Genome Biology</i> , 2012 , 13, 249	18.3	109
267	Role of recently evolved miRNA regulation of sunflower HaWRKY6 in response to temperature damage. <i>New Phytologist</i> , 2012 , 195, 766-773	9.8	86
266	Natural variation in <i>Arabidopsis</i> : from molecular genetics to ecological genomics. <i>Plant Physiology</i> , 2012 , 158, 2-22	6.6	258
265	High-resolution experimental and computational profiling of tissue-specific known and novel miRNAs in <i>Arabidopsis</i> . <i>Genome Research</i> , 2012 , 22, 163-76	9.7	120
264	On epigenetics and epistasis: hybrids and their non-additive interactions. <i>EMBO Journal</i> , 2012 , 31, 249-503		5
263	Reading the second code: mapping epigenomes to understand plant growth, development, and adaptation to the environment. <i>Plant Cell</i> , 2012 , 24, 2257-61	11.6	11
262	Independent FLC mutations as causes of flowering-time variation in <i>Arabidopsis thaliana</i> and <i>Capsella rubella</i> . <i>Genetics</i> , 2012 , 192, 729-39	4	34
261	Plant secondary siRNA production determined by microRNA-duplex structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2461-6	11.5	175

260	1001 Proteomes: a functional proteomics portal for the analysis of Arabidopsis thaliana accessions. <i>Bioinformatics</i> , 2012 , 28, 1303-6	7.2	16
259	Launching eLife, Part 1. <i>ELife</i> , 2012 , 1, e00270	8.9	7
258	Launching eLife, Part 2. <i>ELife</i> , 2012 , 1, e00365	8.9	3
257	Spontaneous epigenetic variation in the Arabidopsis thaliana methylome. <i>Nature</i> , 2011 , 480, 245-9	50.4	533
256	miRNA control of vegetative phase change in trees. <i>PLoS Genetics</i> , 2011 , 7, e1002012	6	281
255	Whole-genome sequencing of multiple Arabidopsis thaliana populations. <i>Nature Genetics</i> , 2011 , 43, 956-63	56.3	737
254	Argonaute10 as a miRNA locker. <i>Cell</i> , 2011 , 145, 173-4	56.2	19
253	ceRNAs: miRNA target mimic mimics. <i>Cell</i> , 2011 , 147, 1431-2	56.2	42
252	What developmental biologists can learn from plant pathogens. <i>Developmental Cell</i> , 2011 , 20, e2	10.2	1
251	Developmental genetics and new sequencing technologies: the rise of nonmodel organisms. <i>Developmental Cell</i> , 2011 , 21, 65-76	10.2	21
250	Fast-forward genetics enabled by new sequencing technologies. <i>Trends in Plant Science</i> , 2011 , 16, 282-8	13.1	169
249	MicroRNA networks and developmental plasticity in plants. <i>Trends in Plant Science</i> , 2011 , 16, 258-64	13.1	253
248	LOCAS--a low coverage assembly tool for resequencing projects. <i>PLoS ONE</i> , 2011 , 6, e23455	3.7	18
247	The Arabidopsis lyrata genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011 , 43, 476-81	36.3	638
246	A major QTL controls susceptibility to spinal curvature in the curveback guppy. <i>BMC Genetics</i> , 2011 , 12, 16	2.6	13
245	Gene duplication and divergence of long wavelength-sensitive opsin genes in the guppy, <i>Poecilia reticulata</i> . <i>Journal of Molecular Evolution</i> , 2011 , 72, 240-52	3.1	41
244	Double-strand break repair processes drive evolution of the mitochondrial genome in Arabidopsis. <i>BMC Biology</i> , 2011 , 9, 64	7.3	152
243	Efficient branch-and-bound techniques for two-locus association mapping. <i>BMC Bioinformatics</i> , 2011 , 12,	3.6	1

242	Negative regulation of anthocyanin biosynthesis in Arabidopsis by a miR156-targeted SPL transcription factor. <i>Plant Cell</i> , 2011 , 23, 1512-22	11.6	568
241	Genetic architecture of flowering-time variation in Arabidopsis thaliana. <i>Genetics</i> , 2011 , 188, 421-33	4	128
240	Reference-guided assembly of four diverse Arabidopsis thaliana genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10249-54	11.5	190
239	Comparative analysis of non-autonomous effects of tasiRNAs and miRNAs in Arabidopsis thaliana. <i>Nucleic Acids Research</i> , 2011 , 39, 2880-9	20.1	78
238	Transposable elements and small RNAs contribute to gene expression divergence between Arabidopsis thaliana and Arabidopsis lyrata. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 2322-7	11.5	247
237	RNA 3Rprocessing functions of Arabidopsis FCA and FPA limit intergenic transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 8508-13	11.5	58
236	Prediction of regulatory interactions from genome sequences using a biophysical model for the Arabidopsis LEAFY transcription factor. <i>Plant Cell</i> , 2011 , 23, 1293-306	11.6	124
235	Evolution of the S-locus region in Arabidopsis relatives. <i>Plant Physiology</i> , 2011 , 157, 937-46	6.6	45
234	Genome-wide comparison of nucleotide-binding site-leucine-rich repeat-encoding genes in Arabidopsis. <i>Plant Physiology</i> , 2011 , 157, 757-69	6.6	141
233	Paired-end RAD-seq for de novo assembly and marker design without available reference. <i>Bioinformatics</i> , 2011 , 27, 2187-93	7.2	79
232	Complex evolutionary events at a tandem cluster of Arabidopsis thaliana genes resulting in a single-locus genetic incompatibility. <i>PLoS Genetics</i> , 2011 , 7, e1002164	6	51
231	Control of lateral organ development and flowering time by the Arabidopsis thaliana MADS-box Gene AGAMOUS-LIKE6. <i>Plant Journal</i> , 2010 , 62, 807-16	6.9	82
230	Genome-wide single nucleotide polymorphisms reveal population history and adaptive divergence in wild guppies. <i>Molecular Ecology</i> , 2010 , 19, 968-84	5.7	116
229	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. <i>Nature</i> , 2010 , 465, 627-31	50.4	1257
228	Natural allelic variation underlying a major fitness trade-off in Arabidopsis thaliana. <i>Nature</i> , 2010 , 465, 632-6	50.4	273
227	Ten years of genetics and genomics: what have we achieved and where are we heading?. <i>Nature Reviews Genetics</i> , 2010 , 11, 723-33	30.1	50
226	Probing the reproducibility of leaf growth and molecular phenotypes: a comparison of three Arabidopsis accessions cultivated in ten laboratories. <i>Plant Physiology</i> , 2010 , 152, 2142-57	6.6	110
225	The role of the Arabidopsis morning loop components CCA1, LHY, PRR7, and PRR9 in temperature compensation. <i>Plant Cell</i> , 2010 , 22, 3650-61	11.6	115

224	STIMPY mediates cytokinin signaling during shoot meristem establishment in Arabidopsis seedlings. <i>Development (Cambridge)</i> , 2010 , 137, 541-9	6.6	59
223	Arabidopsis and relatives as models for the study of genetic and genomic incompatibilities. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010 , 365, 1815-23	5.8	25
222	MicroRNA gene evolution in Arabidopsis lyrata and Arabidopsis thaliana. <i>Plant Cell</i> , 2010 , 22, 1074-89	11.6	204
221	Identification of a spontaneous frame shift mutation in a nonreference Arabidopsis accession using whole genome sequencing. <i>Plant Physiology</i> , 2010 , 153, 652-4	6.6	39
220	Global effects of the small RNA biogenesis machinery on the Arabidopsis thaliana transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17466-73	11.5	57
219	Local-scale patterns of genetic variability, outcrossing, and spatial structure in natural stands of Arabidopsis thaliana. <i>PLoS Genetics</i> , 2010 , 6, e1000890	6	142
218	The scale of population structure in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2010 , 6, e1000843	6	251
217	AGRONOMICS1: a new resource for Arabidopsis transcriptome profiling. <i>Plant Physiology</i> , 2010 , 152, 487-99	6.6	56
216	Natural diversity in flowering responses of Arabidopsis thaliana caused by variation in a tandem gene array. <i>Genetics</i> , 2010 , 186, 263-76	4	28
215	A collection of target mimics for comprehensive analysis of microRNA function in Arabidopsis thaliana. <i>PLoS Genetics</i> , 2010 , 6, e1001031	6	295
214	Transient assays for the analysis of miRNA processing and function. <i>Methods in Molecular Biology</i> , 2010 , 592, 255-64	1.4	32
213	Transmission electron microscopy (TEM) freeze substitution of plant tissues. <i>Cold Spring Harbor Protocols</i> , 2010 , 2010, pdb.prot4959	1.2	6
212	Control of cell proliferation in Arabidopsis thaliana by microRNA miR396. <i>Development (Cambridge)</i> , 2010 , 137, 103-12	6.6	362
211	Climate change and the integrity of science. <i>Science</i> , 2010 , 328, 689-90	33.3	116
210	On reconciling the interactions between APETALA2, miR172 and AGAMOUS with the ABC model of flower development. <i>Development (Cambridge)</i> , 2010 , 137, 3633-42	6.6	172
209	Transcriptional control of gene expression by microRNAs. <i>Cell</i> , 2010 , 140, 111-22	56.2	361
208	Directed gene silencing with artificial microRNAs. <i>Methods in Molecular Biology</i> , 2010 , 592, 71-88	1.4	50
207	The rate and molecular spectrum of spontaneous mutations in Arabidopsis thaliana. <i>Science</i> , 2010 , 327, 92-4	33.3	752

206	Increased leaf size: different means to an end. <i>Plant Physiology</i> , 2010 , 153, 1261-79	6.6	172
205	Small RNAs in flower development. <i>European Journal of Cell Biology</i> , 2010 , 89, 250-7	6.1	14
204	Structure determinants for accurate processing of miR172a in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2010 , 20, 42-8	6.3	124
203	Comprehensive analysis of <i>Arabidopsis</i> expression level polymorphisms with simple inheritance. <i>Molecular Systems Biology</i> , 2009 , 5, 242	12.2	20
202	Cis-regulatory changes at FLOWERING LOCUS T mediate natural variation in flowering responses of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009 , 183, 723-32, 1S1-7S1	4	95
201	Dual roles of the bZIP transcription factor PERIANTHIA in the control of floral architecture and homeotic gene expression. <i>Development (Cambridge)</i> , 2009 , 136, 1613-20	6.6	80
200	The NGATHA genes direct style development in the <i>Arabidopsis</i> gynoecium. <i>Plant Cell</i> , 2009 , 21, 1394-409	6.6	98
199	Linkage analysis reveals the independent origin of Poeciliid sex chromosomes and a case of atypical sex inheritance in the guppy (<i>Poecilia reticulata</i>). <i>Genetics</i> , 2009 , 182, 365-74	4	55
198	Regulation and functional specialization of small RNA-target nodes during plant development. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 622-7	9.9	90
197	Deep sequencing to reveal new variants in pooled DNA samples. <i>Human Mutation</i> , 2009 , 30, 1703-12	4.7	68
196	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. <i>Plant Journal</i> , 2009 , 57, 184-94	6.9	56
195	Highly specific gene silencing by artificial microRNAs in the unicellular alga <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2009 , 58, 165-74	6.9	278
194	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009 , 58, 1068-82	6.9	249
193	Triggering the formation of tasiRNAs in <i>Arabidopsis thaliana</i> : the role of microRNA miR173. <i>EMBO Reports</i> , 2009 , 10, 264-70	6.5	97
192	Selective epigenetic control of retrotransposition in <i>Arabidopsis</i> . <i>Nature</i> , 2009 , 461, 427-30	50.4	260
191	SHOREmap: simultaneous mapping and mutation identification by deep sequencing. <i>Nature Methods</i> , 2009 , 6, 550-1	21.6	451
190	Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 12273-8	11.5	499
189	Quick miniprep for plant DNA isolation. <i>Cold Spring Harbor Protocols</i> , 2009 , 2009, pdb.prot5179	1.2	12

188	miR156-regulated SPL transcription factors define an endogenous flowering pathway in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2009 , 138, 738-49	56.2	925
187	The sequential action of miR156 and miR172 regulates developmental timing in <i>Arabidopsis</i> . <i>Cell</i> , 2009 , 138, 750-9	56.2	1064
186	A genetic defect caused by a triplet repeat expansion in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2009 , 323, 1060-333.3	56	
185	Simultaneous alignment of short reads against multiple genomes. <i>Genome Biology</i> , 2009 , 10, R98	18.3	178
184	The 1001 genomes project for <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2009 , 10, 107	18.3	325
183	Phenotypic analysis of <i>Arabidopsis</i> mutants: bacterial pathogens. <i>Cold Spring Harbor Protocols</i> , 2009 , 2009, pdb.prot4983	1.2	2
182	Genetic linkage map of the guppy, <i>Poecilia reticulata</i> , and quantitative trait loci analysis of male size and colour variation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009 , 276, 2195-208	4.4	90
181	Recent speciation of <i>Capsella rubella</i> from <i>Capsella grandiflora</i> , associated with loss of self-incompatibility and an extreme bottleneck. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 5246-51	11.5	170
180	Dellaporta miniprep for plant DNA isolation. <i>Cold Spring Harbor Protocols</i> , 2009 , 2009, pdb.prot5178	1.2	7
179	QTL mapping in new <i>Arabidopsis thaliana</i> advanced intercross-recombinant inbred lines. <i>PLoS ONE</i> , 2009 , 4, e4318	3.7	77
178	Evolution of metal hyperaccumulation required cis-regulatory changes and triplication of HMA4. <i>Nature</i> , 2008 , 453, 391-5	50.4	638
177	Next-generation genetics in plants. <i>Nature</i> , 2008 , 456, 720-3	50.4	327
176	The impact of shared ancestral variation on hybrid male lethality--a 16 codon indel in the <i>Drosophila simulans</i> Lhr gene. <i>Journal of Evolutionary Biology</i> , 2008 , 21, 551-5	2.3	7
175	Gene silencing in plants using artificial microRNAs and other small RNAs. <i>Plant Journal</i> , 2008 , 53, 674-906.9	531	
174	Genetic analysis of <i>Arabidopsis</i> mutants. <i>Cold Spring Harbor Protocols</i> , 2008 , 2008, pdb.top35	1.2	15
173	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008 , 9, R112	18.3	85
172	Criteria for annotation of plant MicroRNAs. <i>Plant Cell</i> , 2008 , 20, 3186-90	11.6	992
171	The impact of <i>Arabidopsis</i> on human health: diversifying our portfolio. <i>Cell</i> , 2008 , 133, 939-43	56.2	79

170	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8795-800	11.5	297
169	Fixation, embedding, and sectioning of plant tissues. <i>Cold Spring Harbor Protocols</i> , 2008 , 2008, pdb.prot4941	4.1	4
168	A zinc knuckle protein that negatively controls morning-specific growth in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17193-8	11.5	58
167	Detecting polymorphic regions in <i>Arabidopsis thaliana</i> with resequencing microarrays. <i>Genome Research</i> , 2008 , 18, 918-29	9.7	46
166	Correction for Filiault et al., Amino acid polymorphisms in <i>Arabidopsis phytochrome B</i> cause differential responses to light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8482-8482	11.5	78
165	Control of jasmonate biosynthesis and senescence by miR319 targets. <i>PLoS Biology</i> , 2008 , 6, e230	9.7	602
164	Amino acid polymorphisms in <i>Arabidopsis phytochrome B</i> cause differential responses to light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 3157-62	11.5	85
163	Evolution of <i>Arabidopsis thaliana</i> microRNAs from random sequences. <i>Rna</i> , 2008 , 14, 2455-9	5.8	110
162	Sequencing of natural strains of <i>Arabidopsis thaliana</i> with short reads. <i>Genome Research</i> , 2008 , 18, 2024-33	9.7	390
161	Dual effects of miR156-targeted SPL genes and CYP78A5/KLUH on plastochron length and organ size in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2008 , 20, 1231-43	11.6	370
160	Comparative analysis of the MIR319a microRNA locus in <i>Arabidopsis</i> and related Brassicaceae. <i>Molecular Biology and Evolution</i> , 2008 , 25, 892-902	8.3	61
159	Specific gene silencing by artificial MicroRNAs in <i>Physcomitrella patens</i> : an alternative to targeted gene knockouts. <i>Plant Physiology</i> , 2008 , 148, 684-93	6.6	96
158	Highly specific gene silencing by artificial miRNAs in rice. <i>PLoS ONE</i> , 2008 , 3, e1829	3.7	250
157	Transcript normalization and segmentation of tiling array data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008 , 527-38	1.3	8
156	Move on up, it's time for change--mobile signals controlling photoperiod-dependent flowering. <i>Genes and Development</i> , 2007 , 21, 2371-84	12.6	333
155	Common sequence polymorphisms shaping genetic diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007 , 317, 338-42	33.3	596
154	Target mimicry provides a new mechanism for regulation of microRNA activity. <i>Nature Genetics</i> , 2007 , 39, 1033-7	36.3	1445
153	Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2007 , 39, 1151-5	36.3	400

152	Hybrid necrosis: autoimmunity as a potential gene-flow barrier in plant species. <i>Nature Reviews Genetics</i> , 2007 , 8, 382-93	30.1	322
151	ESTs and EST-linked polymorphisms for genetic mapping and phylogenetic reconstruction in the guppy, <i>Poecilia reticulata</i> . <i>BMC Genomics</i> , 2007 , 8, 269	4.5	19
150	HUA2 caused natural variation in shoot morphology of <i>A. thaliana</i> . <i>Current Biology</i> , 2007 , 17, 1513-9	6.3	41
149	Opsin gene duplication and diversification in the guppy, a model for sexual selection. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007 , 274, 33-42	4.4	65
148	Genome-wide patterns of single-feature polymorphism in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12057-62	11.5	147
147	Autoimmune response as a mechanism for a Dobzhansky-Muller-type incompatibility syndrome in plants. <i>PLoS Biology</i> , 2007 , 5, e236	9.7	391
146	Distinct expression patterns of natural antisense transcripts in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2007 , 144, 1247-55	6.6	78
145	MSQT for choosing SNP assays from multiple DNA alignments. <i>Bioinformatics</i> , 2007 , 23, 2784-7	7.2	39
144	Combinations of WOX activities regulate tissue proliferation during <i>Arabidopsis</i> embryonic development. <i>Developmental Biology</i> , 2007 , 309, 306-16	3.1	120
143	Antagonistic regulation of PIN phosphorylation by PP2A and PINOID directs auxin flux. <i>Cell</i> , 2007 , 130, 1044-56	56.2	530
142	Sequence and expression differences underlie functional specialization of <i>Arabidopsis</i> microRNAs miR159 and miR319. <i>Developmental Cell</i> , 2007 , 13, 115-25	10.2	306
141	<i>Arabidopsis</i> : a model genus for speciation. <i>Current Opinion in Genetics and Development</i> , 2007 , 17, 500-4	4.9	34
140	The evolution of selfing in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007 , 317, 1070-2	33.3	132
139	In vitro culture of embryos of the guppy, <i>Poecilia reticulata</i> . <i>Developmental Dynamics</i> , 2006 , 235, 617-22	2.9	20
138	Temperature Induced Flowering in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2006 , 1, 227-8	2.5	34
137	CrossLink: visualization and exploration of sequence relationships between (micro) RNAs. <i>Nucleic Acids Research</i> , 2006 , 34, W400-4	20.1	1
136	NUBBIN and JAGGED define stamen and carpel shape in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2006 , 133, 1645-55	6.6	112
135	Potent induction of <i>Arabidopsis thaliana</i> flowering by elevated growth temperature. <i>PLoS Genetics</i> , 2006 , 2, e106	6	389

134	Identification of plant microRNA homologs. <i>Bioinformatics</i> , 2006 , 22, 359-60	7.2	161
133	Highly specific gene silencing by artificial microRNAs in Arabidopsis. <i>Plant Cell</i> , 2006 , 18, 1121-33	11.6	1007
132	A tiny helper lightens the maternal load. <i>Cell</i> , 2006 , 124, 1117-8	56.2	3
131	The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of Arabidopsis thaliana. <i>Nature Genetics</i> , 2006 , 38, 711-5	36.3	171
130	A divergent external loop confers antagonistic activity on floral regulators FT and TFL1. <i>EMBO Journal</i> , 2006 , 25, 605-14	13	337
129	Evolutionary divergence of LFY function in the mustards Arabidopsis thaliana and Leavenworthia crassa. <i>Plant Molecular Biology</i> , 2006 , 62, 279-89	4.6	19
128	Setting up Arabidopsis crosses. <i>Cold Spring Harbor Protocols</i> , 2006 , 2006,	1.2	17
127	In planta transformation of Arabidopsis. <i>Cold Spring Harbor Protocols</i> , 2006 , 2006,	1.2	24
126	Specific effects of microRNAs on the plant transcriptome. <i>Developmental Cell</i> , 2005 , 8, 517-27	10.2	1178
125	Integration of spatial and temporal information during floral induction in Arabidopsis. <i>Science</i> , 2005 , 309, 1056-9	33.3	1015
124	Conservation and divergence of microRNA families in plants 2005 , 6, P13		58
123	A gene expression map of Arabidopsis thaliana development. <i>Nature Genetics</i> , 2005 , 37, 501-6	36.3	2016
122	Requirement of homeobox gene STIMPY/WOX9 for Arabidopsis meristem growth and maintenance. <i>Current Biology</i> , 2005 , 15, 436-40	6.3	183
121	The 35S promoter used in a selectable marker gene of a plant transformation vector affects the expression of the transgene. <i>Planta</i> , 2005 , 221, 523-30	4.7	120
120	Conservation and divergence of FCA function between Arabidopsis and rice. <i>Plant Molecular Biology</i> , 2005 , 58, 823-838	4.6	44
119	Diversity of flowering responses in wild Arabidopsis thaliana strains. <i>PLoS Genetics</i> , 2005 , 1, 109-18	6	259
118	FRIGIDA-independent variation in flowering time of natural Arabidopsis thaliana accessions. <i>Genetics</i> , 2005 , 170, 1197-207	4	128
117	Comprehensive interaction map of the Arabidopsis MADS Box transcription factors. <i>Plant Cell</i> , 2005 , 17, 1424-33	11.6	414

116	Natural variation in Arabidopsis. How do we find the causal genes?. <i>Plant Physiology</i> , 2005 , 138, 567-8	6.6	82
115	The floral regulator LEAFY evolves by substitutions in the DNA binding domain. <i>Science</i> , 2005 , 308, 260-333	33.3	157
114	A genetic framework for fruit patterning in Arabidopsis thaliana. <i>Development (Cambridge)</i> , 2005 , 132, 4687-96	6.6	99
113	Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 2460-5	11.5	167
112	Haplotype structure and phenotypic associations in the chromosomal regions surrounding two Arabidopsis thaliana flowering time loci. <i>Genetics</i> , 2004 , 168, 1627-38	4	63
111	The role of JAGGED in shaping lateral organs. <i>Development (Cambridge)</i> , 2004 , 131, 1101-10	6.6	229
110	Temporally and spatially controlled induction of gene expression in Arabidopsis thaliana. <i>Plant Journal</i> , 2004 , 38, 164-71	6.9	65
109	From tough nuts to touch-me-nots. <i>Cell</i> , 2004 , 116, 763-4	56.2	6
108	Acceleration of flowering by overexpression of MFT (MOTHER OF FT AND TFL1). <i>Molecules and Cells</i> , 2004 , 17, 95-101	3.5	93
107	Regulatory elements of the floral homeotic gene AGAMOUS identified by phylogenetic footprinting and shadowing. <i>Plant Cell</i> , 2003 , 15, 1296-309	11.6	182
106	Control of leaf morphogenesis by microRNAs. <i>Nature</i> , 2003 , 425, 257-63	50.4	1393
105	A thermosensory pathway controlling flowering time in Arabidopsis thaliana. <i>Nature Genetics</i> , 2003 , 33, 168-71	36.3	355
104	Dissection of floral induction pathways using global expression analysis. <i>Development (Cambridge)</i> , 2003 , 130, 6001-12	6.6	353
103	Large-scale identification of single-feature polymorphisms in complex genomes. <i>Genome Research</i> , 2003 , 13, 513-23	9.7	307
102	Modes of intercellular transcription factor movement in the Arabidopsis apex. <i>Development (Cambridge)</i> , 2003 , 130, 3735-45	6.6	178
101	Genome-wide insertional mutagenesis of Arabidopsis thaliana. <i>Science</i> , 2003 , 301, 653-7	33.3	4165
100	The F-box-containing protein UFO and AGAMOUS participate in antagonistic pathways governing early petal development in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8571-6	11.5	65
99	The extent of linkage disequilibrium in Arabidopsis thaliana. <i>Nature Genetics</i> , 2002 , 30, 190-3	36.3	393

98	Signaling in plants by intercellular RNA and protein movement. <i>Genes and Development</i> , 2002 , 16, 151-8	12.6	73
97	Ectopic expression of SUPERMAN suppresses development of petals and stamens. <i>Plant and Cell Physiology</i> , 2002 , 43, 52-7	4.9	38
96	Independent control of gibberellin biosynthesis and flowering time by the circadian clock in Arabidopsis. <i>Plant Physiology</i> , 2002 , 130, 1770-5	6.6	64
95	Building beauty: the genetic control of floral patterning. <i>Developmental Cell</i> , 2002 , 2, 135-42	10.2	182
94	Interaction of LEAFY, AGAMOUS and TERMINAL FLOWER1 in maintaining floral meristem identity in Arabidopsis. <i>Development (Cambridge)</i> , 2002 , 129, 2519-2527	6.6	102
93	Quantitative trait loci controlling light and hormone response in two accessions of Arabidopsis thaliana. <i>Genetics</i> , 2002 , 160, 683-96	4	101
92	Interaction of LEAFY, AGAMOUS and TERMINAL FLOWER1 in maintaining floral meristem identity in Arabidopsis. <i>Development (Cambridge)</i> , 2002 , 129, 2519-27	6.6	48
91	Functional divergence of the TFL1-like gene family in Arabidopsis revealed by characterization of a novel homologue. <i>Genes To Cells</i> , 2001 , 6, 327-36	2.3	111
90	Natural variation in light sensitivity of Arabidopsis. <i>Nature Genetics</i> , 2001 , 29, 441-6	36.3	229
89	Arabidopsis genome: life without notch. <i>Current Biology</i> , 2001 , 11, R112-4	6.3	23
88	Evolution of floral meristem identity genes. Analysis of Lolium temulentum genes related to APETALA1 and LEAFY of Arabidopsis. <i>Plant Physiology</i> , 2001 , 125, 1788-801	6.6	123
87	NFL1, a Nicotiana tabacum LEAFY-like gene, controls meristem initiation and floral structure. <i>Plant and Cell Physiology</i> , 2001 , 42, 1130-9	4.9	82
86	Transcriptional networks controlling plant development. <i>Plant Physiology</i> , 2001 , 125, 109-11	6.6	15
85	A role for flavin monooxygenase-like enzymes in auxin biosynthesis. <i>Science</i> , 2001 , 291, 306-9	33.3	885
84	A molecular link between stem cell regulation and floral patterning in Arabidopsis. <i>Cell</i> , 2001 , 105, 793-802	36.2	529
83	GAMYB-like Genes, Flowering, and Gibberellin Signaling in Arabidopsis. <i>Plant Physiology</i> , 2001 , 127, 1682-1693	25.0	250
82	Transformation of Medicago truncatula via infiltration of seedlings or flowering plants with Agrobacterium. <i>Plant Journal</i> , 2000 , 22, 531-41	6.9	211
81	Integration of floral inductive signals in Arabidopsis. <i>Nature</i> , 2000 , 404, 889-92	50.4	382

80	Transformation of rice with the Arabidopsis floral regulator LEAFY causes early heading. <i>Transgenic Research</i> , 2000 , 9, 223-7	3.3	43
79	Activation tagging in Arabidopsis. <i>Plant Physiology</i> , 2000 , 122, 1003-13	6.6	813
78	Natural variation in phytochrome signaling. <i>Seminars in Cell and Developmental Biology</i> , 2000 , 11, 523-307.5		27
77	Regulation of auxin response by the protein kinase PINOID. <i>Cell</i> , 2000 , 100, 469-78	56.2	419
76	Cell-cell signaling and movement by the floral transcription factors LEAFY and APETALA1. <i>Science</i> , 2000 , 289, 779-82	33.3	282
75	Independent regulation of flowering by phytochrome B and gibberellins in Arabidopsis. <i>Plant Physiology</i> , 1999 , 120, 1025-32	6.6	87
74	The Arabidopsis flowering-time gene LUMINIDEPENDENS is expressed primarily in regions of cell proliferation and encodes a nuclear protein that regulates LEAFY expression. <i>Plant Journal</i> , 1999 , 18, 195-203	6.9	63
73	The Arabidopsis thaliana MERISTEM LAYER 1 promoter specifies epidermal expression in meristems and young primordia. <i>Plant Journal</i> , 1999 , 20, 259-63	6.9	242
72	Activation of a floral homeotic gene in Arabidopsis. <i>Science</i> , 1999 , 285, 585-7	33.3	326
71	Activation tagging of the floral inducer FT. <i>Science</i> , 1999 , 286, 1962-5	33.3	1126
70	Redundant enhancers mediate transcriptional repression of AGAMOUS by APETALA2. <i>Developmental Biology</i> , 1999 , 216, 260-4	3.1	58
69	A genetic framework for floral patterning. <i>Nature</i> , 1998 , 395, 561-6	50.4	444
68	From floral induction to floral shape. <i>Current Opinion in Plant Biology</i> , 1998 , 1, 55-9	9.9	21
67	Plant development: the making of a leaf. <i>Current Biology</i> , 1998 , 8, R643-5	6.3	3
66	Genetic ablation of flowers in transgenic Arabidopsis. <i>Plant Journal</i> , 1998 , 15, 799-804	6.9	49
65	Patterning the floral meristem. <i>Seminars in Cell and Developmental Biology</i> , 1998 , 9, 221-6	7.5	14
64	Gibberellins promote flowering of arabidopsis by activating the LEAFY promoter. <i>Plant Cell</i> , 1998 , 10, 791-800	11.6	437
63	Gibberellins Promote Flowering of Arabidopsis by Activating the LEAFY Promoter. <i>Plant Cell</i> , 1998 , 10, 791	11.6	3

62	Flowering-time genes modulate the response to LEAFY activity. <i>Genetics</i> , 1998 , 150, 403-10	4	134
61	A LEAFY co-regulator encoded by UNUSUAL FLORAL ORGANS. <i>Current Biology</i> , 1997 , 7, 95-104	6.3	240
60	Flower development: repressing reproduction. <i>Current Biology</i> , 1997 , 7, R373-5	6.3	1
59	Modulating the timing of flowering. <i>Current Opinion in Biotechnology</i> , 1997 , 8, 195-9	11.4	34
58	Sizing Up the Floral Meristem. <i>Plant Physiology</i> , 1996 , 112, 5-10	6.6	25
57	Cell-cell interactions: taking cues from the neighbors. <i>Current Biology</i> , 1996 , 6, 10-2	6.3	5
56	A developmental switch sufficient for flower initiation in diverse plants. <i>Nature</i> , 1995 , 377, 495-500	50.4	674
55	The APETALA2 Domain Is Related to a Novel Type of DNA Binding Domain. <i>Plant Cell</i> , 1995 , 7, 388	11.6	16
54	The genetics of flower development: from floral induction to ovule morphogenesis. <i>Annual Review of Genetics</i> , 1995 , 29, 19-39	14.5	156
53	Sp1/egr-like zinc-finger protein required for endoderm specification and germ-layer formation in <i>Drosophila</i> . <i>Nature</i> , 1994 , 369, 664-8	50.4	115
52	Plant development. The SEcReTs of Arabidopsis embryogenesis. <i>Current Biology</i> , 1994 , 4, 1040-2	6.3	2
51	The ABCs of floral homeotic genes. <i>Cell</i> , 1994 , 78, 203-9	56.2	864
50	Activation of floral homeotic genes in Arabidopsis. <i>Science</i> , 1993 , 261, 1723-6	33.3	258
49	Patterning the Arabidopsis embryo. <i>Current Biology</i> , 1993 , 3, 443-5	6.3	8
48	Leafy Controls Meristem Identity in Arabidopsis 1993 , 115-122		6
47	LEAFY controls floral meristem identity in Arabidopsis. <i>Cell</i> , 1992 , 69, 843-59	56.2	1237
46	Floral patterning. <i>Current Opinion in Genetics and Development</i> , 1991 , 1, 174-8	4.9	12
45	A genetic and molecular model for flower development in Arabidopsis thaliana. <i>Development (Cambridge)</i> , 1991 , 113, 157-167	6.6	69

44	Two gap genes mediate maternal terminal pattern information in <i>Drosophila</i> . <i>Science</i> , 1990 , 248, 495-8	33.3	196
43	Regulation of Krüppel expression in the anlage of the Malpighian tubules in the <i>Drosophila</i> embryo. <i>Mechanisms of Development</i> , 1990 , 33, 57-67	1.7	39
42	The fork head domain: a novel DNA binding motif of eukaryotic transcription factors?. <i>Cell</i> , 1990 , 63, 455-6	56.2	417
41	Primordium specific requirement of the homeotic gene fork head in the developing gut of the <i>Drosophila</i> embryo. <i>Roux's Archives of Developmental Biology</i> , 1989 , 198, 201-210		50
40	The homeotic gene fork head encodes a nuclear protein and is expressed in the terminal regions of the <i>Drosophila</i> embryo. <i>Cell</i> , 1989 , 57, 645-58	56.2	661
39	Novel homeotic genes in <i>Drosophila melanogaster</i> . <i>Biochemistry and Cell Biology</i> , 1989 , 67, 393-6	3.6	6
38	Terminal versus segmental development in the <i>Drosophila</i> embryo: the role of the homeotic gene fork head. <i>Roux's Archives of Developmental Biology</i> , 1988 , 197, 345-354		62
37	The <i>Drosophila</i> homolog of the mouse mammary oncogene int-1 is identical to the segment polarity gene wingless. <i>Cell</i> , 1987 , 50, 649-57	56.2	789
36	Molecular organization of master mind, a neurogenic gene of <i>Drosophila melanogaster</i> . <i>Molecular Genetics and Genomics</i> , 1987 , 207, 374-384		12
35	Correction: The rise and fall of the <i>Phytophthora infestans</i> lineage that triggered the Irish potato famine. <i>ELife</i> , 2,	8.9	5
34	Adaptive diversification of growth allometry in the plant <i>Arabidopsis thaliana</i>		1
33	Modulation of ACD6 dependent hyperimmunity by natural alleles of an <i>Arabidopsis thaliana</i> NLR resistance gene		1
32	RST1 and RIPR connect the cytosolic RNA exosome to the Ski complex in <i>Arabidopsis</i>		1
31	Oligomerization of NLR immune receptor RPP7 triggered by atypical resistance protein RPW8/HR as ligand		4
30	An ultra high-density <i>Arabidopsis thaliana</i> crossover map that refines the influences of structural variation and epigenetic features		1
29	The rate and potential relevance of new mutations in a colonizing plant lineage		1
28	A role for the F-box protein HAWAIIAN SKIRT in plant miRNA function		2
27	High contiguity <i>Arabidopsis thaliana</i> genome assembly with a single nanopore flow cell		7

26	The genetic architecture of recurrent segregation distortion in <i>Arabidopsis thaliana</i>	3
25	An Algorithm to Build a Multi-genome Reference	2
24	A singleton NLR of recent origin causes hybrid necrosis in <i>Arabidopsis thaliana</i>	1
23	Host-associated microbe PCR (hamPCR): accessing new biology through convenient measurement of both microbial load and community composition	4
22	Mutation bias shapes gene evolution in <i>Arabidopsis thaliana</i>	7
21	CRISPR-finder: A high throughput and cost effective method for identifying successfully edited <i>A. thaliana</i> individuals	1
20	Drainage-structuring of ancestral variation and a common functional pathway shape limited genomic convergence in natural high- and low-predation guppies	2
19	<i>Arabidopsis</i> cell surface LRR immune receptor signaling through the EDS1-PAD4-ADR1 node	12
18	Image-based methods for phenotyping growth dynamics and fitness components in <i>Arabidopsis thaliana</i>	4
17	Stability of association between <i>Arabidopsis thaliana</i> and <i>Pseudomonas</i> pathogens over evolutionary time scales	1
16	Incomplete reprogramming of cell-specific epigenetic marks during asexual reproduction leads to heritable phenotypic variation in plants	1
15	A map of climate change-driven natural selection in <i>Arabidopsis thaliana</i>	3
14	Long-term balancing selection drives evolution of immunity genes in <i>Capsella</i>	1
13	Multiple modes of convergent adaptation in the spread of glyphosate-resistant <i>Amaranthus tuberculatus</i>	3
12	The <i>Arabidopsis thaliana</i> pan-NLRome	6
11	RPW8/HR Repeats Predict NLR-dependent Hybrid Performance	5
10	Specific Regulation of TCP genes by miR319	1
9	Position-dependent effects of cytosine methylation on FWA expression in <i>Arabidopsis thaliana</i>	2

8	Combining whole genome shotgun sequencing and rDNA amplicon analyses to improve detection of microbe-microbe interaction networks in plant leaves	5
7	The relationship between microbial population size and disease in the <i>Arabidopsis thaliana</i> phyllosphere	15
6	DNA sequence properties that predict susceptibility to epiallelic switching	2
5	Genotyping-by-sequencing-based identification of <i>Arabidopsis</i> pattern recognition receptor RLP32 recognizing proteobacterial translation initiation factor IF1	2
4	Protective host-dependent antagonism among <i>Pseudomonas</i> in the <i>Arabidopsis</i> phyllosphere	1
3	Contrasting patterns of microbial dominance in the <i>Arabidopsis thaliana</i> phyllosphere	2
2	Homozygosity at its Limit: Inbreeding Depression in Wild <i>Arabidopsis arenosa</i> Populations	1
1	Small peptides modulate the immune function of the ion channel-like protein ACD6 in <i>Arabidopsis thaliana</i>	1